

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 12, 2002, 13:02:34 : Search time 1593 Seconds
(without alignments)
3304.339 Million cell updates/sec

Title: US-09-818-954A-2
Perfect score: 390
Sequence: 1 atgaagctgcgtctctctc.....ccacgagctgtgagaccac 390

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlmu:*
5: em_estlov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	286.2	73.4	680	9	BB624070 BB624070
2	188	48.2	405	12	AQ495547 HS-5211.B
3	176.6	45.3	560	10	BM262079 dag40d11.
4	171.2	43.9	617	9	BE131943 db40d09.Y
5	168.2	43.1	635	10	BM262389 dag40d11.
6	72.6	18.6	928	12	CNS0201E
7	57.8	14.8	285	12	BH327754 CH230-117
8	53	13.6	1355	11	AK017593 Mus muscu
9	50.8	13.0	592	12	BH279786 CH230-108
10	49.8	12.8	423	10	BG379148 UI-R-BT1-
11	49.8	12.8	497	9	BE102709 UI-R-BT1-
12	49.4	12.7	434	10	BI033915 OV2-NN200
13	48.8	12.5	606	9	AV754501 AV754501
14	48.2	12.4	372	10	BF398865 UI-R-CAL-
15	47.8	12.3	452	9	AV746068 AV746068
16	47.8	12.3	268	12	AZ871616 2M0184002
17	47.8	12.3	522	9	AV173269 AV173269

18	47.8	12.3	523	9	BB618381
19	47.8	12.3	546	10	BF074571 222022 MA
20	47.8	12.3	584	10	BM224915 K0203E03-
21	47.4	12.2	584	10	BM224971 K0204C05-
22	47.2	12.1	453	9	A1051683 oy77h08.x
23	47.2	12.1	560	9	AV752236 AV752236
24	47.2	12.1	678	9	AV751658 AV751658
25	46.4	11.9	328	10	BF079065 229583 MA
26	46.4	11.9	379	10	BF442180 258778 MA
27	46.4	11.9	409	10	BE749737 200773 MA
28	46.4	11.9	414	10	BF075383 224374 MA
29	46.4	11.9	476	10	BF442020 258543 MA
30	46.4	11.9	482	10	BF080835 231861 MA
31	46.4	11.9	515	10	BI343866 372161 MA
32	46.4	11.9	516	10	BI345127 373848 MA
33	46.4	11.9	516	10	BF702350 M1-P-A2-a
34	46.4	11.9	527	10	BI339266 364172 MA
35	46.4	11.9	625	9	AV753384 AV753384
36	45.8	11.7	634	9	AV745740 AV745740
37	45.4	11.6	481	9	A1189453 qd02c08.x
38	45.4	11.6	525	9	A1148695 qc38904.x
39	45	11.5	544	9	A1148647 qc69a08.x
40	44.8	11.5	519	9	A1149163 qc76a04.x
41	44.6	11.4	447	9	A1291937 qm81c01.x
42	44	11.3	433	9	AV748886 AV748886
43	44	11.3	487	10	BF190158 236616 MA
44	44	11.3	539	9	A1188964 qd22b08.x
45	43.8	11.2	446	9	A1276216 q176b05.x

ALIGNMENTS

RESULT 1
LOCUS BB624070
DEFINITION BB624070 RIKEN full-length enriched, adult male eyeball Mus musculus cDNA clone 7530426119 5', mRNA sequence.
ACCSSION BB624070
VERSION BB624070.1 GI:16462680
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE
AUTHORS
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Iehli,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koye,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)

TITLE
JOURNAL
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagui,K., Fujiwaka,S., Inoue,K., Togawa,Y., Itawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

QY 323 CCTATCCCGGCGCATCCGCTGTGACTGCGAGCGCTCTCCATCGCCACCGAGGTGTG 382
 |||||
 Db 142 CCGATCCCGGCGCATCCGCTGTGACTGCGAGCGCTCTCCATCGCCACCGAGGTGTG 201
 |||||
 QY 383 AGACCATC 390
 |||||
 Db 202 AGACCATC 209

RESULT 3
 BM262079 560 bp mRNA linear EST 18-DEC-2001
 LOCUS daq40d11.x3 Blackshear/Soares normalized Xenopus egg library
 DEFINITION Xenopus laevis cDNA clone IMAGE:4783917 3' similar to SW:GTHB_CYPCA
 P01235 GONADOTROPIN BETA CHAIN PRECURSOR. [1]; mRNA sequence.
 ACCESSION BM262079
 VERSION BM262079.1 GI:17925119
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 560)
 Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Page,D.,
 Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
 ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
 Waterston,R. and Wilson,R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)
 CONTACT: Sandy Clifton, Ph.D.
 Washu Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by Bento Soares and M. Fatima Bonaldo
 (University of Iowa). DNA sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LNL at: info@image.lnl.gov
 Seq primer: -40UP from GIBCO
 High quality sequence stop: 473.
 Location/Qualifiers
 1..560
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:4783917"
 /clone_lib="Blackshear/Soares normalized Xenopus egg
 library"
 /sex="female"
 /tissue_type="unfertilized egg"
 /cell_type="unfertilized egg"
 /dev_stage="unfertilized egg"
 /lab_host="DH10B"
 /note="Vector: pT73-Pac; Site 1: EcoRI; Site 2: NotI;
 polyA-selected mRNA was prepared from unfertilized Xenopus
 laevis eggs. The library was constructed in the vector
 pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
 Soares, M.B. 'Normalization and subtraction: two
 approaches to facilitate gene discovery', Genome Research
 6:791-806, 1996. The first strand synthesis used a
 NotI-drf18 primer; double stranded cDNAs were ligated to
 EcoRI adaptors, digested with NotI, and directionally
 cloned into the NotI and EcoRI-digested pT73-Pac vector.
 The library contained approximately 7.2 x 10⁵
 recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT 164 a 112 c 120 g 164 t

ORIGIN

Query Match 45.3%; Score 176.6; DB 10; Length 560;
 Best Local Similarity 73.0%; Pred. No. 1.e-34;

Matches 227; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 76 TTCAGTGGGAACTGGCGACCTTTGTGGGCTGTGCTCCGAGGAGATTACTTCTGGCC 135
 |||||
 Db 543 TTCATATATAGCTGAGAAACGTTGATGTGCTGTGAGGGAATTCATTCTTACA 484
 |||||
 QY 136 AAGAAGCCAGGCTGAGGAGGCTTGCAGTACACAGAGATGCTGGGGCTGTGAG 195
 |||||
 Db 483 AAGAAGCTGGCTGACAGAGGCTGTGCTGTGACTACTGATGCTGCTGGGGGCGCTGTAG 424
 |||||
 QY 196 ACCTGGGAGAAACCATTTCTGGAACCCCTATATTGAAGCCATCATCATGCTGTACC 255
 |||||
 Db 423 ACCTGGGAGAAACCATTCCTGATATCCCTGATACATAGAAAGCCACACAGAGTGTGACT 364
 |||||
 QY 256 TACACAGACCAACACAGGTACTGTCAAGTGCACCAACTGTGCCCGGAGTGCACCC 315
 |||||
 Db 363 TACATGAACTAACTGATGCTGTAATAAGTGCACCAACTGCAGCCAGACATTTGACCA 304
 |||||
 QY 316 TTCTACACCTATCCCGGCGCATCCGCTGTGAGTGCAGGAGCGCTGCCTGACATGCCACAG 375
 |||||
 Db 303 TTCTTTACCTACCCACGATGGTCCATTAGATGTGACTGTGACATTTGTTCCACTTTACTACA 244
 |||||
 QY 376 GAGGTGTGAGAC 386
 |||||
 Db 243 GAATGTGAGAC 233

RESULT 4
 BE131943 617 bp mRNA linear EST 29-JUN-2000
 LOCUS da40d09.y1 Blackshear/Soares normalized Xenopus egg library
 DEFINITION Xenopus laevis cDNA clone IMAGE:3300977 5' similar to SW:GTHB_CYPCA
 P01235 GONADOTROPIN BETA CHAIN PRECURSOR. [2] SW:GTHB_CYPCA; mRNA
 sequence.
 BE131943
 BE131943.1 GI:8579306
 VERSION EST.
 KEYWORDS African clawed frog.
 SOURCE Xenopus laevis
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 617)
 Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Page,D.,
 Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
 ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
 Waterston,R. and Wilson,R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)
 CONTACT: Sandy Clifton, Ph.D.
 Washu Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by Bento Soares and M. Fatima Bonaldo
 (University of Iowa). DNA sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LNL at: info@image.lnl.gov
 Seq primer: -40RP from GIBCO
 High quality sequence stop: 467.
 Location/Qualifiers
 1..617
 /organism="Xenopus laevis"
 /db_xref="taxon:8355"
 /clone="IMAGE:3300977"
 /clone_lib="Blackshear/Soares normalized Xenopus egg
 library"
 /sex="female"
 /tissue_type="unfertilized egg"
 /cell_type="unfertilized egg"

FEATURES
 SOURCE

```

/dev_stage="unfertilized egg"
/lab_host="DH10B"
/notes="vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subcloning: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-drl8 primer: double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT7T3-Pac vector.
The library contained approximately 7.2 x 106
recombinants, with average insert sizes of 1-1.5 kb."

```

Query Match	43.9%	Score 171.2	DB 9	Length 617
Best Local Similarity	67.9%	Pred. No. 2.6e-33		
Matches 239	Conservative	0	Mismatches 113	Indels 0
			Gaps	0

QY	30	CATGGCCCTCCCTCCCTTTCGGCGGTATGGCTGTGTCTCCGGTGGCTCCAGTGGGAACCT	89
Db	266	CCTGAGGCTTCGGCTTTTAGCCCTGTGTCTCAGCAACCCGCTCAGAGTCCAAATATAACTCT	325
QY	90	GGCACCCTTTGGGCTCTGCCGTGAGGAGACTTTACTTCTTCGGCCAAAGAACCCAGCTCG	149
Db	326	GAGAAACGTTTCATTGGATGGCTGTGTAGGGAAATTCACATTTCTTTAGCAAAACAAACCTGGCTG	385
QY	150	CAGGGGCCCTTGGGATCACCACACGAGATCCCTGCCTGGGGGTGCTGTGAGACCTGGGAGAAAC	209
Db	386	CAGAGCTCTGGCGTGTGACTACTGATGGCTCGTGGGGCGCGCTGTGAACTGTGAGAGGCC	445
QY	210	CATTCTGGAACCCCCCTATTTGGAAGCCCATATGAGTCTGTACTACACGAGACCAA	269
Db	446	ATCCCTAAATCCCTCCGTACATAGAAGCCCCACACAGAGCTCTCACTTACAAAGAAGAACTAA	505
QY	270	ACAGGTGACTCAAGCTCCACCACTGTGTCGCCGGGAGTGCACCCCTTCTATACACTATCC	329
Db	506	ACTGGTACTGTAAATAGTGCACCAACTGGAGCCCAAGACATTTGACCCTATTTTACTACACC	565
QY	330	CGTGGCCATCCGCTGTGACTGGCGAGACCTGCTTCACACTGCACACACAGGAGTGT	381
Db	566	AGTTGCCCATTAATATGTGACTGTGACATGTGTGTCACACTTCTTACTAAGAAATGT	617

RESULT 5
BM262389

LOCUS
DEFINITION

BM262389 635 bp mRNA linear EST 18-DEC-2001
dag40d11.y3 Blackshear/Soares normalized Xenopus egg library
Xenopus laevis cDNA clone IMAGE:478317 5' similar to SW:GTRB_CYPCL
P01235 GNADOTROPIN BETA CHAIN PRECURSOR. [1] ; mRNA sequence.

ACCESSION
VERSION
KEYWORDS

BM262389
BM262389.1 GI:17925429
EST.

SOURCE
ORGANISM

African clawed frog.
Xenopus laevis

REFERENCE

1 (bases 1 to 635)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,
B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
Washu Xenopus EST Project, 1999
Unpublished (1999)
Other_ESTs: dag40d11.x3
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800

FEATURES
Source Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by Bento Soares and M. Fatima Bonaldo
 (University of Iowa). DNA Sequencing by: Washington University
 Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 491.
 Location/Qualifiers
 1. .635

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/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:4783917"
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/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH10B"
/note="Vector: pT73-Pac; Site.1: EcoRI; Site.2: NotI.
PolyA-selected mRNA was prepared from unfertilized Xenopus
laevis eggs. The library was constructed in the vector
pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
Soares, M.B. 'Normalization and subtraction: two
approaches to facilitate gene discovery', Genome Research
6:791-806, 1996. The first strand synthesis used a
NotI-dT18 primer; double stranded cDNAs were ligated to
EcoRI adapters, digested with NotI, and directionally
cloned into the NotI and EcoRI-digested pT73-Pac vector.
The library contained approximately 7.2 x 105
recombinants, with average insert sizes of 1-1.5 kb."

```

	Query Match	43.1%	Score 168.2;	DB 10;	Length 635;
	Best Local Similarity	68.3%;	Pred. No. 1.5e-32;		
Matches 233;	Conservative	0;	Mismatches 108;	Indels	Gaps
Oy	30 CATGCGCCCTCCTCCTTCGTGGCTATGAGTGTGTCTCTCGTGACCTCCAGTGGGAACCT	89			
Db	295 CCTGCAGCTTCTGTGTTTAGCCCTGTGTCTCAGCACCGCTCAGAGATCAATTATAAGTCT	354			
Oy	90 GCGCACCTTTGTGGGCTGTGCCGTGAGGAGTTACTTTCTTGCCAAAGAACCAGCTG	149			
Db	355 GAGAACGTTCAATTGGATGTGCTGTGAGGGAAATTCACATTTTACCAAAGAAACCTGGCTG	414			
Oy	150 CAGGGGCTTGGAMTCACAGSANTGCTGTGGGTGCGTGTAGACTGTGGGAAGAAC	209			
Db	415 CAGAGGTCTGTGGTGTGACTGATGCTGTGTGGGGGGCTGTAGACTGTGGGAAGACC	474			
Oy	210 CATTCGTGAACCCCCCTATTATTGAAGCCATCATTCGATGTGTATCTCAACAGAACCA	269			
Db	475 ATCCCTAGATCTCTCCGTRCATAGAAAGCCACACAGATCTGCACATTGCAATGAACAATA	534			
Oy	270 ACAGAGTACTGTCAAGCTGCCAACCTGTGCCCGSGAGTGCAGCCCTTCTACACCTATCC	329			
Db	535 ACTGCTTACTGTAAACATGCCAAGCTGAGGCCAGACATGACCACTCTTACTTACC	594			
Oy	330 CGTGGCCATCCGCTGTGTACTCGGAGCCTGCTCCACATGCCA	370			
Db	595 AGTTGCCATTGATGTGACTGTGACATTTGTTCACATTTCTA	635			

RESULT 6	CNS20201E/c	928 bp	DNA	linear	GSS 14-MAY-2000
LOCUS	CNS20201E				
DEFINITION	Petiodon nigroviridis genome survey sequence 17 end of clone 15213 of library G from Tetraodon nigroviridis, genomic survey sequence.				
ACCESSION	AL206123				
VERSION	AL206123.1				GI:7864942

Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhaot@igr.org Clones are derived from the rat BAC library CHOR1-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Plietier de Jong (pdejong@emall.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orienting/information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 117 row: A column: 17 Seq primer: T7 Class: BAC ends.	
FEATURES	location/Qualifiers
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	/organism="Rattus norvegicus"
	/strain="BN/SSNHsd/MKW"
	/db_xref="taxon:10116"
	/clone="CH230-117A17"
	/clone_id="CHOR1-230 Segment 1"
	/sex="Female"
	/cell_type="Brain"
	/note="Vector: pPARAC2.1; Site_1: EcoRI; Site_2: KcoRI; CHOR1-230 Rat (BN/SSNHsd/MKW) BAC library produced by Plietier de Jong"
BASE COUNT	60 a 66 c 83 g 76 t
ORIGIN	
Query Match	14.8%; Score 57.8; DB 12; Length 285;
Best Local Similarity	96.7%; Pred. No. 0.00013;
Matches	59; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	144 AGGCTGCAGGGGCGCTTGCGATCACACAGGAGCCGTCGGTGGCTGAGACCTGGCA 203
Db	1 AGGCTGCAGGGGCGCTTGCGATCACACAGAGCTCTGCGGTGCTGTGAGACCTGGCA 60
OY	204 G 204
Db	61 G 61
RESULT 8	
AKO17593	1595 bp mRNA linear HTC 19-JAN-2002
LOCUS	Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730420N04:follicle stimulating hormone beta, full insert sequence.
ACCESSION	AKO17593
VERSION	AKO17593.1 GI:12856911
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain:C57Bl/6J) 8 days embryo cDNA to mRNA, clone_id:RIKEN full-length enriched mouse cDNA library clone:5730420N04. Mus musculus Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ORGANISM	
REFERENCE	
AUTHORS	1 (sites)
TITLE	Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
JOURNAL	
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2 (sites)
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
JOURNAL	
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3 (sites)

clone was derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_SEO=None found"

	92 a	102 c	147 g	82 t
ch	12.8%	Score 49.8;	DB 10;	Length 423;
1 Similarity	55.5%;	Pred. No. 0.015;		
96; Conservative	0;	Mismatches 77;	Indels 0;	Gaps 0;

CTGTGACACCCCGCTATATTGAAGCCCATATGAGTCTGTACTACAAGACCACAAC 271
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTGTGCAGTCGTCCTGGCTGCCCTCCGCTCAGCACAGTGTCACACTGAGTGCGC 274
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
GTGACATCGCGCTGTGACTGCGGAGACCTGTCCACTGCCCACACGAGTGTGAG 384
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
GGSCCTTCAGACGCTCCGCTGTGGGCCCTGCCGCTCACTAGACTGTGACTGGG 161
| | | | | | | | | | | | | | | | | | | | | | | | | | | |

BE102709 497 bp mRNA linear EST_13-JUN-2000
UI-R-BRI-aqp-b-11-0-UI.s1 UI-R-BRI Rattus norvegicus cDNA clone
BE102709
UI-R-BRI-aqp-b-11-0-UI 3', mRNA sequence.
BE102709.1 GI:8494808
EST.

Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 497)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonalde poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized corpus-striatum library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)

Seq primer: M13 Forward
POLY-A-Tes.

Location/Qualifiers
1..497
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-BRI-aqp-b-11-0-UI"
/clone_lib="UI-R-BRI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/note="Vector: PT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
UI-R-BRI is a subtracted library derived from a mixture of

BASE COUNT	92 a	102 c	147 g	82 t
ORIGIN				
Query Match	12.8%	Score 49.8;	DB 10;	Length 423;
Best Local Similarity	55.5%;	Pred. No. 0.015;		
Matches	96; Conservative	0; Mismatches	77; Indels	0; Gaps
OY	212	TTCTGGAGACCCCTATATTGTAAGCCCATCATGCAGTGTGTACTACACAGACCAAAC	271	
Db	333	TACTGACCGAGTCGCTTGCTCCCTCGCTCCGACCAAGTAGTGAACCTACGTCGCGC	274	
OY	272	AGTGACATGTACACTGTCGCCCAACTGTGTGCCCGGGAGTGCAGCCCTTACACATATCCCG	331	
Db	273	TCGCGCTGTGTCCGCTCCCTCGCTGCGTACCCTGTGTGAGACCCCATAGTCTTCCTTTCTG	214	
OY	332	TGGCCATCCGCTGTGACTGTGCGAGACCTGCTCACCTGCACACGAGAGTGTAG	384	
Db	213	TGGCGCTGACGCTGCGCGCTGTGTGGCCGCTGCCTGACAGAGCTGTGACGTGTGG	161	
RESULT 11				
BEI02709/c	497 bp mRNA linear ESR 13-JUN-2000			
LOCUS	UI-R-BT1-agp-b-11-0-UI.s1 UI-R-BT1 Rattus norvegicus cDNA clone			
DEFINITION	UI-R-BT1-agp-b-11-0-UI 3', mRNA sequence.			
ACCESSION	BEI02709			
VERSION	BEI02709.1 GI:8494808			
KEYWORDS	EST.			
SOURCE	Norway rat.			
ORGANISM	Rattus norvegicus; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 497) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (9), 791-806 (1996)			
JOURNAL	Contact: Soares, MB			
MEDLINE	Program for Rat Gene Discovery and Mapping			
COMMENT	University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel.: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.uiowa.edu The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the Oligo-dT track served to identify it as a clone from the normalized corpus-striatum library cDNA library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) Seq primer: M13 Forward POLYA=yes.			
FEATURES	Location/Qualifiers			
SOURCE	1..497 /organism="Rattus norvegicus" /strain="Sprague-Dawley" /db_xref="taxon:10116" /clone="UI-R-BT1-agp-b-11-0-UI" /clone_1id="UI-R-BT1" /dev_stage="adult" /lab_host="DH10B (Life Technologies)" /note="Vector: pUT73D-pac (Pharmacia) with a modified polylinker. Site_1: Not I; Site_2: Eco RI; The library UI-R-BT1 is a subtracted library derived from a mixture of			

us-09-818-954a-2.rst

Matches	80: Conservative	0: Mismatches	52: Indels	0: Gaps	0:
OY	230	TGTACTTCAACAGACCAACAGTGTACTGTCAAGTGTCCCACTGTGCCCGGAGATC	309		
Db	207	TGTACTTCAACAGCAAGTGTATGTAAACAGTGAAGAGCCCGGTGTCTCACCATTC	266		
OY	310	GACCCCTCTACACTATTCGCCGTGCGCATTCGCTGTACTGGAGCGCTGCCTCCACTGCC	369		
Db	267	GATTCCTCTGTATACATACCAGTGGCCACCAAGTGTCACTGTGGCAAGTGTACAGGCAC	326		
OY	370	ACCACGAGGTGT 381			
Db	327	AGCACTGATGTGT 338			
RESULT 14	BF398865/c				
LOCUS	BF398865	372 bp	mrna	linear	EST 27-NOV-2000
DEFINITION	UI-R-CAL-bja-a-15-0-UI.s1 UI-R-CAL Rattus norvegicus cDNA clone				
ACCESSION	UI-R-CAL-bja-a-15-0-UI 3', mRNA sequence.				
VERSION	BF398865				
KEYWORDS	BF398865.1 GI:11383867				
SOURCE	EST.				
ORGANISM	Norway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
REFERENCE	1 (bases 1 to 372) Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene discovery Genome Res. 6 (9), 791-806 (1996)				
AUTHORS	Journal MEDLINE COMMENT				
JOURNAL	97044477				
MEDLINE	Contact: Soares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565 Email: msoares@blue.weeg.iowa.edu				
COMMENT	The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus-striatum library cDNA library Preparation: M.B. Soares lab clone distribution: clones will be available through Research Genetics (www.resgen.com) Seq primer: M13 forward POLYA-Yes.				
FEATURES	Location/Qualifiers				
source	1..372 /organism="Rattus norvegicus" /strain="Sprague-Dawley" /db_xref="taxon:10116" /clone="UI-R-CAL-bja-a-15-0-UI" /clone_1id="UI-R-CAL1" /lab_host="DH10B (Life Technologies)" /note="Vector: pRT3D-Pac (Pharmacia) with a modified polylinker: site.1: Not I; Site.2: Eco RI; The UI-R-CAL library is a substracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons , midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratel.stg.uiowa.edu . The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996) TAG_Lib-UI-R-CAL TAG_TISSUE=corpus-striatum TAG_SEQ=CTAGC				
BASE COUNT	88 a 75 c 138 g 71 t				

ORIGIN	Query Match	12.4%	Score 48.2	DB 10	Length 372
Best Local Similarity	54.9%	Pred. No. 0.038			
Matches 95	Conservative	0	Mismatches 78	Indels 0	Gaps 0
OY	212	TTCTGGAACCCCCCATTTGAGAGCCCAATCGAGTGTGATCACTACAAAGACAGCAAC	271		
DB	332	TACTCCACAGTCATATGGCTTCCCGCTCCAGCCAGGTGTGACACTACCGTAGCGCGCT	273		
OY	272	AGTGACGTGTAAGCTGGCCCAACTTGGCCGGGAGTGCAGCCCTTTCACACTATCCCG	331		
DB	272	TGCGCTCTGTCCGCTCCGCTCCGCTCCACACCTGGTGTAGACCCATATCTTCCTTCCGT	213		
OY	332	TGGCCATCCGCTGTGACTGCGGAGCGCTGCTCCACTGACCAACAGGATGTGAG	384		
DB	212	TGGCCCTCAGCTGCGCTGTGTGGCCCTCCGCTCTCAGTAGCTGACTGTGGG	160		
RESULT 15					
AV746068					
LOCUS	AV746068	452 bp	mrna	linear	EST 18-Oct-2000
DEFINITION	AV746068	NPA Homo sapiens cDNA clone NPAAD10 5', mRNA sequence.			
ACCESSION	AV746068				
VERSION	AV746068.1	GI:10865515			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 452)				
TITLE	Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,Y., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q., Han,Z., Chen,Z., Hu,R. and Chen,J.				
JOURNAL	Homo sapiens NPA library cDNA clones				
COMMENT	Unpublished (2000)				
	Contact: Qinghua Zhang				
	Shanghai Institute of Endocrinology, Rui-Jin Hospital				
	197 Rui-Jin II Road, Shanghai 200025, P. R. China				
	Tel: 86-21-64370045(ex.663332)				
	Fax: 86-21-64743206				
	Email: mbshlems.stn.sh.cn				
	This clone is available at Shanghai Hematology Institute in Shanghai.				
FEATURES	Shanghai National Human Genome Center at Shanghai				
source	351 Guo Loujing Road, Zhangjiang Hi-Tech Park, Pudong.				
	Location/Qualifiers				
	1..452				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="NPAAD10"				
	/clone_lib="NPA"				
	/tissue_type="pituitary"				
	/dev_stage="Adult"				
	/lab_host="SOLR"				
	/note="Vector: pbluescript sk(-); Site_1: EcoRI; Site_2: XhoI"				
BASE COUNT	58 a	177 c	122 g	91 t	4 others
ORIGIN					
Query Match	12.3%	Score 48	DB 9	Length 452	
Best Local Similarity	57.1%	Pred. No. 0.045			
Matches 84	Conservative	0	Mismatches 63	Indels 0	Gaps 0
OY	238	CATCATGAGTGTGATCTACAAAGACAAACAGGATGATGTGACACTGCCAAGTGT	297		
DB	166	CCTCAGGTGTGTGACCTACCGGTATGTGGCGCTTCAGAGTCATCCGGCTCCCTGGCTGC	245		
OY	238	GCCCCGGAAGTGCAGCCCTTCTACACCTATCCCGGCCCATCCGCTGTGACTGGAGCC	357		
DB	246	CCGCGTGGNGTGGACCCGCTGTCTCTCCCTGCGTCTCAGCTGTGCGTGTGAGGAGCC	305		

QY 358 TGCTCCACTGCGACGAGGTGTGAG 384
||| |
Db 306 TGCCGCCGNNAGCCTCTGTGACTGTGGG 332

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